

## Exercise 1.1

### Single locus models

Assume a 1 locus model with 2 alleles, and the genotypic means are as in the Notes, i.e,  $G_{11} = 320$ ;  $G_{12} = 310$  and  $G_{22} = 280$ .

- Determine breeding value and genetic value for each of the genotypes if the allele frequency for A1 is equal to 0.5.
- Make a Table in Excel, where Genetic Value and Breeding Value for each genotype depend on the gene frequency and the genotypic means.
- Calculate also the population mean and the average effects of each allele for each configuration.
- Derive formulae to find the optimal allele frequency to optimize the maximum population mean (at this frequency).
- Make a graph of average population merit against gene frequency
- Make a graph of average effects plotted against gene frequency,
- (At this stage you can copy a pre-fabricated Excel file (SINGLOC) that uses a Visual Basic-macro to make graphs. You can change any value in the yellow area (genotypic means), and with ctrl\_d the macro will run the graphs for all gene frequencies)

### From genes to distributions

This question uses the program LOCI (from GENUP) to demonstrate how normal distribution of genetic values can be approached when a sufficient number of loci are involved in the trait of interest. It also illustrates that normality is not achieved under certain circumstances. Normality is a basic assumption of much selection theory.

It is assumed for simplicity that each locus has just two alleles, that the a- value (deviation of the better homozygote from the average of homozygotes) and the d- value (deviation of the heterozygote from the average of homozygotes) are the same for each locus, and that p (the frequency of the better allele) is always the same. All loci are assumed to be independent from each other, i.e. not linked.

The scale for the distribution is marked with ticks at intervals of one predicted standard deviation, and the tick in the middle of the scale is set at the predicted mean. }

- [a.] Set the number of animals, number of loci, a, d and p to (500, 1, 1, 0, 0.5) and let the program run. How many different classes of genetic values result? Are these values as you predict ? (Note that genetic values can only be represented by the class into which they fall, and the midpoint of a class does not necessarily represent accurately the genetic values it contains).

Are the genotype proportions as you would predict - exactly ? - roughly ?  
 Why is the population mean not exactly as predicted ?  
 Is the resulting distribution of values reasonably symmetrical ?

- [b.] Repeat the run, but with only 4 animals: (4, 1, 1, 0, 0.5). Rerun several times with these parameters and observe the importance of stochastic (random) effects in such small populations. Are the genotypic proportions as you would expect, on average?
- [c.] Rerun as before, but with 500 animals and 2 loci: (500, 2, 1, 0, 0.5) How many different genotypes can exist? Why are there only 5 genotypic values represented in the resulting distribution?
- [d.] Make a run with parameters (500, 10, 1, 0, 0.5). What are the lowest and highest values possibly attainable? Are these represented on your histogram? Comment on why this is. Does the distribution look symmetrical and normal?
- [e.] Make a few runs, each with a different number of loci (say 3, 5, 10, and 25), all with 500 animals,  $a=1$ ,  $d=1$  and  $p=0.5$ . Note the extent to which each distribution appears symmetrical.
- [f.] Make a number of runs, each with 500 animals, 10 loci and  $a=1$ , but with  $p$  varying (you can choose the values) and  $d$  having values of 0 or 1. Setting up a 2--way table may help, with the values of  $p$  and  $d$  describing the row and column conditions. For each cell note the extent to which each distribution appears symmetrical.
- [g.] From the results you have had, describe what conditions might cause normality of genetic values not to be quite closely realised.

### Simple selection theory

Run GENUP and load SEL. Note that you can run multiple copies of SEL within GENUP, and resize their windows and click 'Redraw' to compare results on-screen.

1. Try running the program with proportion selected  $p = 0.1$ ,  $h^2 = 0.25$ , and  $S_p = 0.5$  Kg. Note that the distribution of phenotypic values differs in detail between generations. This is what you would expect in real life due to random chance effects, and is generated in the computer the random number generator. What type of distribution is approximated within a generation?

How many generations of selection contribute to the difference between the means of the first and fifth generations? Note that despite notable response, there is still considerable overlap of yearling weights between these generations. There are no deviations in generation environmental effects (such as climatic effects affecting whole generations, not to be confused with the environmental deviation each individual within a generation has), as shown in the bottom graph. Thus in this case, genetic and observed (phenotypic) trends are equal.

Make a note of the total response from generation one to five, by reading from the scale at the bottom of the screen, or by clicking on the 'Results' button. Do another run using exactly the same parameters. You should get a slightly different result (but possibly the same by chance, if so try another run) and the distributions will differ in detail from the previous run. How does this relate to real life? Write both total responses on the board, where a class average will be calculated.

2. Using your last output from question 1, find the approximate value of the selection differential in the first generation. How close is the result to what you would predict? Approximately what proportion of this superiority of parents over their contemporaries was transmitted to the next generation? What have you just estimated? Find the sum of the selection differentials for those generations in which selection contributes to response in generation 5. How close is this value to what you would predict? Divide the total response by this value - what have you just estimated?
3. Calculate the response you would have predicted for question 1 ( $R=i h^2 S_p$  per generation of selection). This value will be compared to the average realised response from the whole room.
4. Rerun as in 1 but with  $p=0.25$ . What does this do to the selection differentials? Can you detect any effect on realised heritability? Would you expect any effect? Calculate a predicted response and compare this with your realised response at generation 5. Note the steadiness in genetic trend - this will be referred to in the next question.
5. Rerun as in 1 but with  $p=0.01$ . What does this do to the selection differentials? Calculate a predicted response and compare this with your realised response at generation 5. You may see a more inconsistent genetic trend (if not this will be because of "good luck", rerun the program until you see this effect). Can you explain what might cause it? (Hint: never put all your eggs in one basket).
6. Rerun as in question 1 but with  $h^2=0$ . Explain the result. Repeat this using  $h^2=1$ , and explain this result.
7. Rerun as in 1 but with  $S_p =.1\text{Kg}$ . Compare your selection differentials and realised response to those from questions 1 and 2, and explain the results. How does this realised response compare to what you would predict?
8. Increase the standard deviation of generation environmental effects from 0 to 0.5Kg. Try a run using the other parameters as in 1. As a farmer running such a selection program, how would you react to the results achieved as the program progresses? Try more than one run. Generation means can be read after clicking the 'Results' button.

Note the steadiness in genetic trends, despite large fluctuations in observed trends.

Genetic trend can be found by subtracting the environmental trend from the observed trend. Can you suggest how the farmer can identify his genetic trend in real life?

9 (by 'hand')

In a mob of 200 sheep (100 of each sex), hogget fleece weight was recorded as a selection criterion. The mean values for rams and ewes were 5.0Kg and 4.5Kg respectively, and the standard deviation was  $\sigma_p = 0.5\text{Kg}$  in each sex.

- [a.] The heaviest fleece from a ram weighed 6.3Kg. Is this close to what you might expect?
- [b.] If  $h^2 = 0.4$ , what is the estimated breeding value of this best ram?
- [c.] If he were mated to a randomly selected mob of ewes, what would be the expected progeny mean? Assume an equal expression of response in each sex, and an equal sex ratio (50:50).
- [d.] If he were mated to all the ewes with fleece weights of 5Kg and over, what would be the expected progeny mean